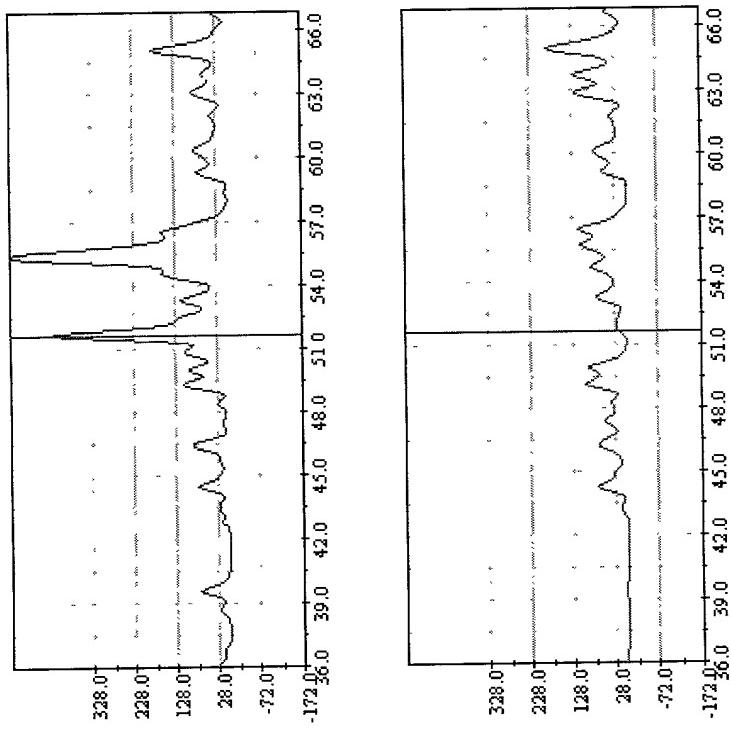


Figure 1



; GAP of: W0h051-7.Seq check: 6926 from: 1 to: 52  
seq of dicamba induced band w0c0 51.7  
to: Cjlp181r.Seq check: 2737 from: 1 to: 714

Symbol comparison table: Gencoredisk: [Gcgcore.Data.Rundata] Nwsgapdma.Cmp  
CompCheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000
Quality:	520	Length:	714
Ratio:	10.000	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

Match display thresholds for the alignment(s) :

WOH051-7. Seg x C1p181r: Seq.: :

1	CGATCGGAAGTGGGTGTCAGCTAGCTTACGGCCTGATCAAGGAAAGTGATCCGATGGAGCTG	51
26	gcttagctggccgtgaccacgcacat	1
27	gaccgcaggcgccggggctgtatca	1
50	CGATCGGAAGTGGGTGTCAGCTAGCTTACGGCCTGATCAAGGAAAGTGATCCGATGGAGCTG	100
52	.	.

Figure 2

SCANNED # 4

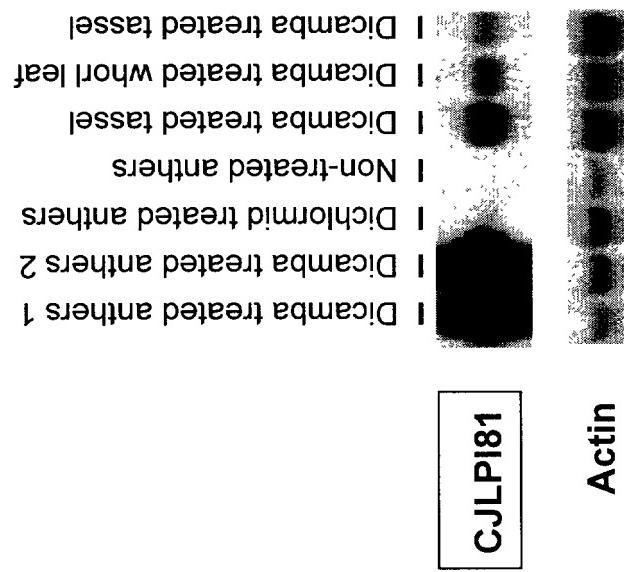


Figure 3

SCANNED,# 4

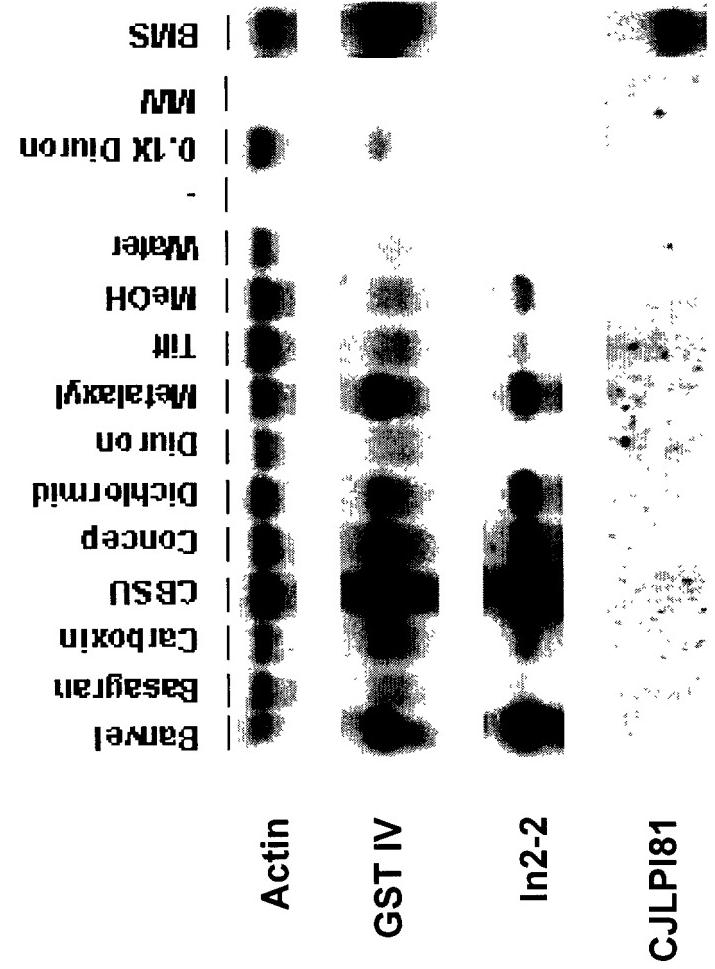


Figure 4

Figure 5

SCANNED# 4

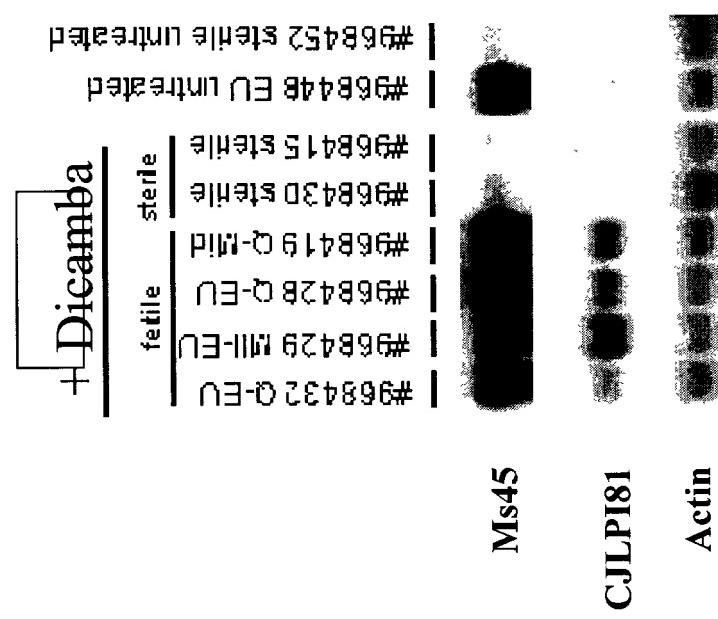
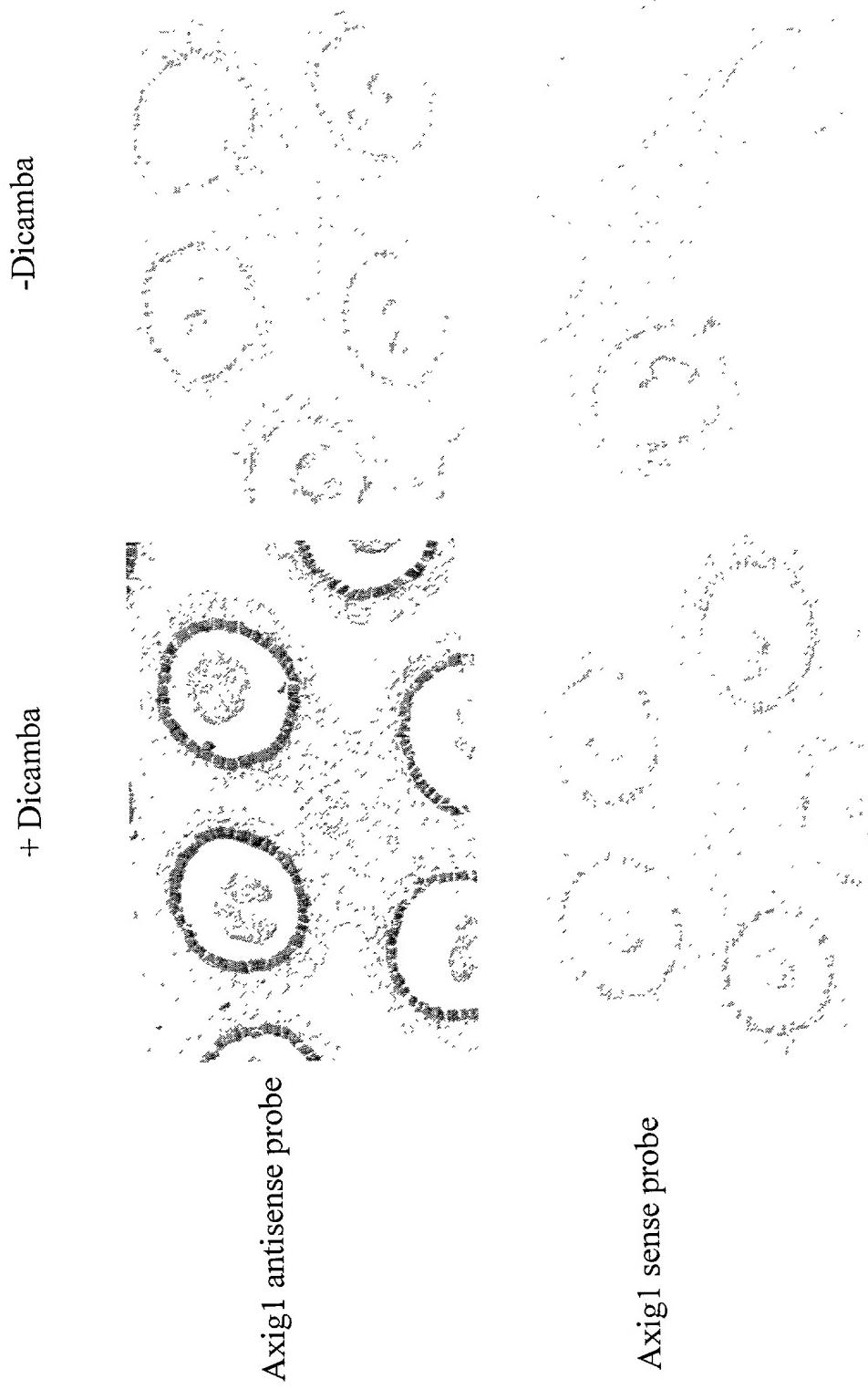


Figure 6

Figure 7



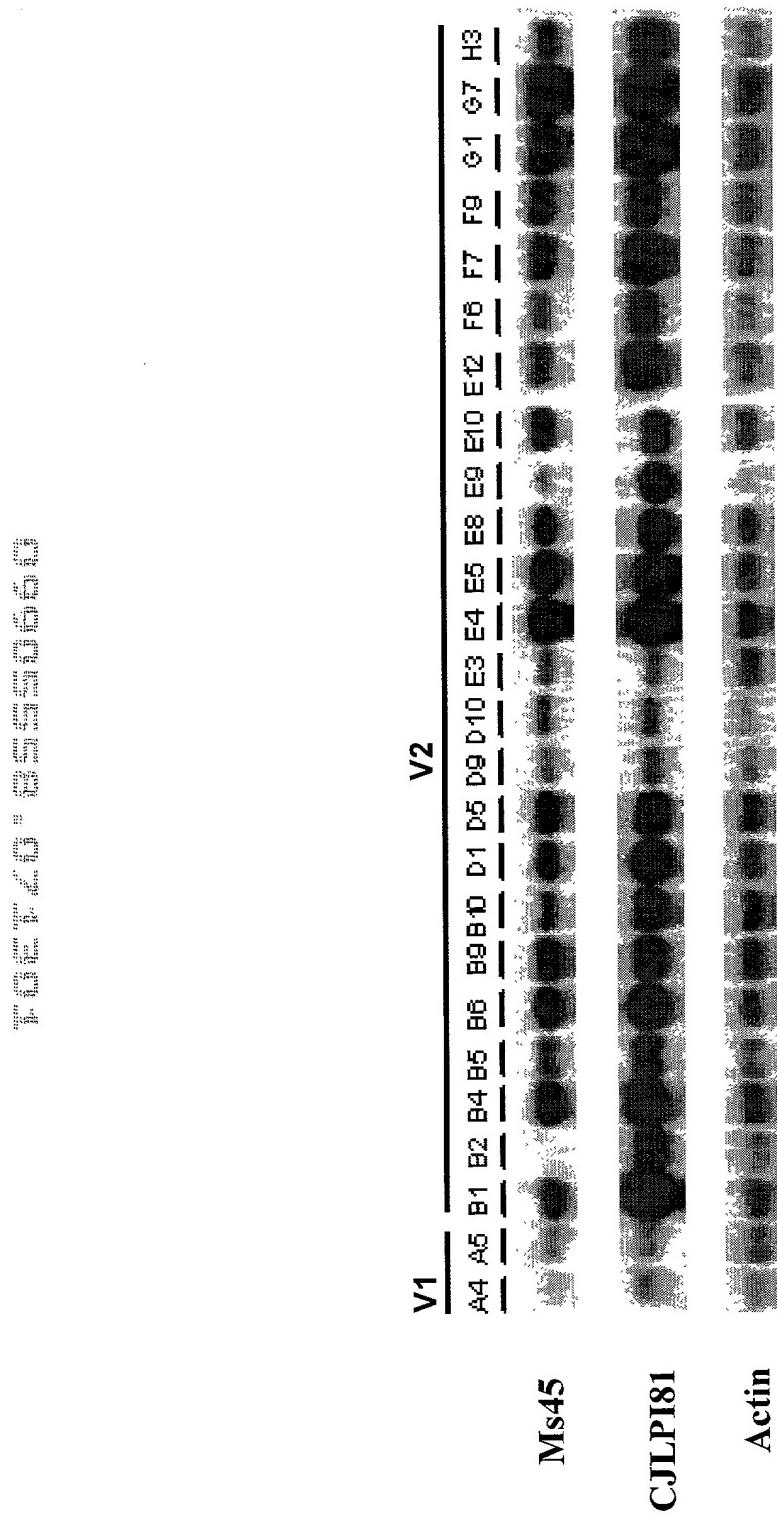


Figure 8

Figure 9

GAP of: Czaal47.Seq check: 446 from: 1 to: 1214  
to: Axiglcomplete.Con check: 928 from: 1 to: 3123

```
Symbol comparison table:  
Gencoredisk: [Gcgcore.Data.Rundata] Nwsgapdna.Cmp  
CompCheck: 8760
```

Gap Weight: 50 Average Match: 10.000  
 Length Weight: 3 Average Mismatch: 0.000  
 Quality: 10871 Length: 3123  
 Ratio: 8.955 Gaps: 3  
 Percent Similarity: 100.000 Percent Identity: 100.000

```
Match display thresholds for the alignment(s):
      | = IDENTITY
      : =    5
      . =    1
```

Czaal47.Seq x Axiglcomplete.Con May 11, 2000 12:05 ...

1 ..... GCAGGAACCTTAT 12  
1101 CGCGTCACTCACGGGTAGCTCATGGTCGAGCGTAGCATGCAGGAACTTAT 1150  
13 TTGCCGTGCGCTCCCAGGTCTCCGCTCGCGTGCCTTCCAGTCTGTCTCAC 62  
1151 TTGCCGTGCGCTCCCAGGTCTCCGCTCGCGTGCCTTCCAGTCTGTCTCAC 1200  
63 ACTAGCTGCTGTGGGACGATCGAAGTGGGTGTGTCAGCTAGCTAGCTGCG 112  
1201 ACTAGCTGCTGTGGGACGATCGAAGTGGGTGTGTCAGCTAGCTAGCTGCG 1250  
113 CCGTGACCACGCACATGACCGCAGTGCAGCGCGGGCTGATCAAGGGAAAG 162  
1251 CCGTGACCACGCACATGACCGCAGTGCAGCGCGGGCTGATCAAGGGAAAG 1300  
163 TGATCGGATGGAGCTGGAGCTCGGGCTCGCCGCCGAACCCGCATCAGC 212  
1301 TGATCGGATGGAGCTGGAGCTCGGGCTCGCCGCCGAACCCGCATCAGC 1350  
213 CGCTGGCTGCCGCCCGAGTTCGTCGGTCTCCTCAGCAGCTCGGCTGGC 262  
1351 CGCTGGCTGCCGCCCGAGTTCGTCGGTCTCCTCAGCAGCTCGGCTGGC 1400  
263 TCGTGCGGAAACAAGAGGGTTCTCGCGACCGTTCGGGCCAAGGC 312  
1401 TCGTGCGGAAACAAGAGGGTTCTCGCGACCGTTCGGGCCAAGGC 1450  
313 GGCCACGCTTCCGCTTCGTCTCGAGGATGGCGACGGAGGCGCGCG 362  
1451 GGCCACGCTTCCGCTTCGTCTCGAGGATGGCGACGGAGGCGCGCG 1500

363 ACCCGCACCGCGACGGCGTCGACCATGAACAGCAAAGCAACAA... 408  
1501 ACCCGCACCGCGACGGCGTCGACCATGAACAGCAAAGCAACAAGTGA 1550

409 ..... TGTACCCAGGAAGAAGAGGCTGG 431  
1601 CCCAAATCCGATCCGTGGTGTGTAGTGTACCCAGGAAGAAGAGGCTGG 1650

432 TGGGGTGGCCGCCCGTGAAGTGCAGCGTAGGCGTAGCTGCGCGCGGG 481  
1651 TGGGGTGGCCGCCCGTGAAGTGCAGCGTAGGCGTAGCTGCGCGCGGG 1700

482 TACGTGAAGGTGAAGCTGGAAGGGTGCCCATCGGGCGGAAGGTGGACGT 531  
1701 TACGTGAAGGTGAAGCTGGAAGGGTGCCCATCGGGCGGAAGGTGGACGT 1750

532 GTCCATCCACGGCTCGTACCAGGAGCTGCTCCGACGCTCGAGAGCATGT 581  
1751 GTCCATCCACGGCTCGTACCAGGAGCTGCTCCGACGCTCGAGAGCATGT 1800

582 TCCCTTCGGGTAACCAACA..... 600  
1801 TCCCTTCGGGTAACCAACAAGGTGCGTACGTTCCCGGGCCGGCGAGCC 1850

601 ..... AG 602  
1951 CTCCCGGCACTTAACTGGTCGCATATACTATTCTGTAACCTCTGGCAG 2000

603 ATCATGCAGAACGAGCAGGGTGGTGGTCTCGCACGAGCGCCCGTCGCCAT 652  
2001 ATCATGCAGAACGAGCAGGGTGGTGGTCTCGCACGAGCGCCCGTCGCCAT 2050

653 CCTTATGTAGTCACCTACGAGGACGGCGAAGGGGACTGGTTGCTCGTCGG 702  
2051 CCTTATGTAGTCACCTACGAGGACGGCGAAGGGGACTGGTTGCTCGTCGG 2100

703 AGATGATGTGCCGTGGGA..... 720  
2101 AGATGATGTGCCGTGGGAGTACGTATCAGTCACTACTGTCGTCTGTA 2150

721 ..... GGTCTTTGTCAGTCAGTG 739  
2201 GAACTAAAAACGACGTTGATTCTCTTGCAGGGTCTTGTCAGTCAGTG 2250

740 AAGCGGCTCAAGATACTTGCAGGGTCTTGTCAGTCAGTG 789  
2251 AAGCGGCTCAAGATACTTGCAGGGTCTTGTCAGTCAGTG 2300

790 GTGTGGTCCGTCTCACCAAGGATCGGAGCAGTGTAGTACTCCTGGCGTCA 839  
|||  
2301 GTGTGGTCCGTCTCACCAAGGATCGGAGCAGTGTAGTACTCCTGGCGTCA 2350

840 TCTGCGTAATAACGTTGTTCTGCCTGTGCCCGTAGCAGTACGTACT 889  
|||  
2351 TCTGCGTAATAACGTTGTTCTGCCTGTGCCCGTAGCAGTACGTACT 2400

890 GTCCTATAGTAAGCTAGCTTATGGGGTGCTTCAGCTTCAGAGCATGAC 939  
|||  
2401 GTCCTATAGTAAGCTAGCTTATGGGGTGCTTCAGCTTCAGAGCATGAC 2450

940 GAAAGCACTGATTAGCTGCTGTCATCACATTGGTCGTCTTGTGTCGT 989  
|||  
2451 GAAAGCACTGATTAGCTGCTGTCATCACATTGGTCGTCTTGTGTCGT 2500

990 ACGGTATCGCTGGCGTCAGTGTGCGGGCAGCCTAGGTGATCTAACGATAC 1039  
|||  
2501 ACGGTATCGCTGGCGTCAGTGTGCGGGCAGCCTAGGTGATCTAACGATAC 2550

1040 TTACTATCTCAAGTTACTTTGGTTCTGAGCTGATGGTAATTCTATA 1089  
|||  
2551 TTACTATCTCAAGTTACTTTGGTTCTGAGCTGATGGTAATTCTATA 2600

1090 TACCGTATACTGTGACTCAGGGCGAAGCTGCCTTAAGGCACAGGGG 1139  
|||  
2601 TACCGTATACTGTGACTCAGGGCGAAGCTGCCTTAAGGCACAGGGG 2650

1140 TCACCGGACCCGATGGAATTATCAAATCCAGTGTAAAATACTATTTAAC 1189  
|||  
2651 TCACCGGACCCGATGGAATTATCAAATCCAGTGTAAAATACTATTTAAC 2700

1190 ACTGTTCATCAATATATTGATTTC..... 1214  
|||  
2701 ACTGTTCATCAATATATTGATTCAATAATTGAGCTGACCTTG 2750

Sequence Name	SEQ ID NO:	ATCC Deposit
Pioneer clone CZAAL47	1	PTA-2426
ZmAxig1 polypeptide	2	
Native ZmAxig1 promoter region	3	
Modified ZmAxig1 promoter region	4	PTA-2427
A632 full-length ZmAxig1, including SEQ ID No. 3	5	PTA-2426 PTA-2427
Primer 1, used for isolation of 5' flanking region	6	
Primer 2, used for isolation of 5' flanking region	7	
Primer 3, used for isolation of region spanning start codon	8	
Primer 4, used for isolation of region spanning start codon	9	
Primer 5, used for isolation of 5' region	10	
Oligonucleotide designed to remove clones having a poly-A tail but no cDNA	11	
Pioneer clone Cjlpi81	12	
CuraGen fragment w0h051.7	13	
Primer 6, used to isolate the coding sequence and 3' region	14	
Primer 7, used to isolate the coding sequence and 3' region	15	
Modified ZmAxig1 promoter region with single-base deletion	16	PTA-2427
LEC1 transcriptional activator element	17	
LEC1 polynucleotides	18-20	
LEC1 polypeptide consensus sequence	21	

**Figure 10.** Representative polynucleotides and polypeptides of the present invention.

Experiment	Control	Ubi:LEC1	Axig1:LEC1
#1 3938.37	15%	63%	44%
#2 3938.79	4%	17%	20%
#3 3938.78	16%	17%	38%
#4 3938.34	2%	14%	13%

**Figure 11.** Transformation frequencies by LEC1 with two different promoters.

Transformation frequencies were based on the percentage of plated embryos with one or more GFP positive/Bialaphos resistant colonies. All embryos were shot with Ubi:moPAT~GFP (a construct conferring Bialaphos resistance and GFP fluorescence) along with a LEC1 construct or a control DNA.